



#6

SEQUENCE LISTING

<110> FARWICK, MIKE
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<120> Nucleotide sequences which code for the sahH gene

<130> 211739US0X

<140> 09/919,854

<141> 2001-08-02

<150> DE 100 44 706.6

<151> 2000-09-09

<150> DE 101 09 685.2

<151> 2001-02-28

<150> US 60/294,277

<151> 2001-05-31

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1939

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (227) .. (1720)

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tggaagaggc agatgtggaa tatgacctcg aagcttattt agaggccctc aactagccct 180

ccactaaaca gtttcaatca attcggtgtc cactccaaca tgtaga gtg gtg cgc 235
Val Val Arg
1

gtt aaa aaa gtt ttc cta att ttc att ttc tta aaa gga gct cgc cag 283
Val Lys Lys Val Phe Leu Ile Phe Ile Phe Leu Lys Gly Ala Arg Gln
5 10 15

gac atg gca cag gtt atg gac ttc aag gtt gcc gat ctt tca cta gca 331
Asp Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala

20	25	30	35	
gag gca gga cgt cac cag att cgt ctt gca gag tat gag atg cca ggt Glu Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly	40	45	50	379
ctc atg cag ttg cgc aag gaa ttc gca gac gag cag cct ttg aag ggc Leu Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly	55	60	65	427
gcc cga att gct ggt tct atc cac atg acg gtc cag acc gcc gtg ctt Ala Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu	70	75	80	475
att gag acc ctc act gct ttg ggc gct gag gtt cgt tgg gct tcc tgc Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys	85	90	95	523
aac att ttc tcc acc cag gat gag gct gca gcg gct atc gtt gtc ggc Asn Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ile Val Val Gly	100	105	110	571
tcc ggc acc gtc gaa gag cca gct ggt gtt cca gta ttc gcg tgg aag Ser Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys	120	125	130	619
ggt gag tca ctg gag gag tac tgg tgg tgc atc aac cag atc ttc agc Gly Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser	135	140	145	667
tgg ggc gat gag ctg cca aac atg atc ctc gac gac ggc ggt gac gcc Trp Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala	150	155	160	715
acc atg gct gtt att cgc ggt cgc gaa tac gag cag gct ggt ctg gtt Thr Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val	165	170	175	763
cca cca gca gag gcc aac gat tcc gat gag tac atc gca ttc ttg ggc Pro Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly	180	185	190	811
atg ctg cgt gag gtt ctt gct gca gag cct ggc aag tgg ggc aag atc Met Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile	200	205	210	859
gct gag gcc gtt aag ggt gtc acc gag gaa acc acc acc ggt gtg cac Ala Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His	215	220	225	907
cgc ctg tac cac ttc gct gaa gaa ggc gtg ctg cct ttc cca gcg atg Arg Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met	230	235	240	955
aac gtc aac gac gct gtc acc aag tcc aag ttt gat aac aag tac ggc Asn Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly	245	250	255	1003

acc cgc cac tcc ctg atc gac ggc atc aac cgc gcc act gac atg ctc Thr Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu 260 265 270 275	1051
atg ggc ggc aag aac gtg ctt gtc tgc ggt tac ggc gat gtc ggc aag Met Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys 280 285 290	1099
ggc tgc gct gag gct ttc gac ggc cag ggc gct cgc gtc aag gtc acc Gly Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr 295 300 305	1147
gaa gct gac cca atc aac gct ctt cag gct ctg atg gat ggc tac tct Glu Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser 310 315 320	1195
gtg gtc acc gtt gat gag gcc atc gag gac gcc gac atc gtg atc acc Val Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr 325 330 335	1243
gcg acc ggc aac aag gac atc att tcc ttc gag cag atg ctc aag atg Ala Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met 340 345 350 355	1291
aag gat cac gct ctg ctg ggc aac atc ggt cac ttt gat aat gag atc Lys Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile 360 365 370	1339
gat atg cat tcc ctg ttg cac cgc gac gac gtc acc cgc acc acg atc Asp Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile 375 380 385	1387
aag cca cag gtc gac gag ttc acc ttc tcc acc ggt cgc tcc atc atc Lys Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile 390 395 400	1435
gtc ctg tcc gaa ggt cgc ctg ttg aac ctt ggc aac gcc acc gga cac Val Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His 405 410 415	1483
cca tca ttt gtc atg tcc aac tct ttc gcc gat cag acc att gcg cag Pro Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln 420 425 430 435	1531
atc gaa ctg ttc caa aac gaa gga cag tac gag aac gag gtc tac cgt Ile Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg 440 445 450	1579
ctg cct aag gtt ctc gac gaa aag gtg gca cgc atc cac gtt gag gct Leu Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala 455 460 465	1627
ctc ggc ggt cag ctc acc gaa ctg acc aag gag cag gct gag tac atc Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile 470 475 480	1675

ggc gtt gac gtt gca ggc cea ttc aag ccg gag cac tac cgc tac 1720
 Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr
 485 490 495

taatgattgt cagcattgag ggaatcgacg gcgccggcaa aaacaccctg gtttcggcat 1780

taacgcaggt tattgatgca aaagtccttg cattcccacg ttatgaaacc tcgattcacg 1840

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<212> PRT

<213> Corynebacterium glutamicum

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Ala Arg Gln Asp Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu
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Ser Leu Ala Glu Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu
 35 40 45

Met Pro Gly Leu Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro
 50 55 60

Leu Lys Gly Ala Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr
 65 70 75 80

Ala Val Leu Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp
 85 90 95

Ala Ser Cys Asn Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile
 100 105 110

Val Val Gly Ser Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe
 115 120 125

Ala Trp Lys Gly Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln
 130 135 140

Ile Phe Ser Trp Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly

145		150		155		160
Gly Asp Ala Thr Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala						
	165			170		175
Gly Leu Val Pro Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala						
	180			185		190
Phe Leu Gly Met Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp						
	195			200		205
Gly Lys Ile Ala Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr						
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Gly Val His Arg Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe						
	225			230		235
Pro Ala Met Asn Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn						
		245		250		255
Lys Tyr Gly Thr Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr						
		260		265		270
Asp Met Leu Met Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp						
	275			280		285
Val Gly Lys Gly Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val						
	290			295		300
Lys Val Thr Glu Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp						
	305			310		315
Gly Tyr Ser Val Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile						
		325		330		335
Val Ile Thr Ala Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met						
		340		345		350
Leu Lys Met Lys Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp						
	355			360		365
Asn Glu Ile Asp Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg						
	370			375		380

Thr Thr Ile Lys Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg
385 390 395 400

Ser Ile Ile Val Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala
405 410 415

Thr Gly His Pro Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr
420 425 430

Ile Ala Gln Ile Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu
435 440 445

Val Tyr Arg Leu Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His
450 455 460

Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala
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Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr
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Arg Tyr

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